

SEQUENCE LISTING

<110> Chang, Gwong-Jen J

<120> Nucleic Acid Vaccines for Prevention of
Flavivirus Infection

<130> 14114.0332U3

<150> PCT/US99/12298

<151> 1999-06-03

<150> 09/701,536

<151> 2000-11-29

<150> 60/087,908

<151> 1998-06-04

<160> 31

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<213> Artificial Sequence

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<223> Description of artificial sequence; note =
synthetic construct

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<222> (25)...(48)

<221> misc_feature

<222> 1-48

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<223> Description of artificial sequence; note =
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14114.0332U3

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<223> Description of artificial sequence; note =
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<223> Description of artificial sequence; note =
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<223> Description of artificial sequence; note =
synthetic construct

<223> pCDJE 2-7

SEQUENCE LISTING

THE
JOURNAL
OF
THE
ROYAL
ANTHROPOLOGICAL
INSTITUTE
OF GREAT
BRITAIN
AND IRELAND
PART 1
1905

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 Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser
 515 520 525
 Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
 530 535 540
 Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
 545 550 555 560
 Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
 565 570 575
 Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
 580 585 590
 Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
 595 600 605
 Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
 610 615 620
 Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
 625 630 635 640
 Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
 645 650 655
 Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
 660 665 670
 Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu
 675 680 685
 Val Phe Leu Ala Thr Asn Val His Ala
 690 695

<210> 12

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of artificial sequence; note =
 synthetic construct

<221> misc_feature

<222> 1-46

<223> WN 466

<400> 12

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<220>
<223> Description of artificial sequence; note =
synthetic construct

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43

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<220>
<223> Description of artificial sequence; note =
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<210> 15
<211> 5308
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of artificial sequence; note =
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<221> CDS
<222> (911) . . . (2987)
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<221> misc_feature
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<223> pCBWN
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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
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 tggagttccg cgttacataa cttacggtaa atggcccgcg tggctgaccg cccaacgacc 360
 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
 attgacgtca atgggtggag tatttacggg aaactgcccc cttggcagta catcaagtgt 480
 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
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 tcgctattac catggtgatg cggtttttgg cagtacatca atgggcgtgg atagcggttt 660
 gactcacggg gatttccaag tctccacccc attgacgtca atgggagttt gttttggcac 720
 caaaatcaac gggactttcc aaaatgtcgt aacaactccg cccattgac gcaaattgggc 780
 ggtaggcgtg tacgggtggga ggtctatata agcagagctc tctggctaac tagagaaccc 840
 actgcttact ggcttatcga aattaatacg actcactata gggagaccca agcttggtac 900
 cgccgcgcgc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg 949
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala
 1 5 10

agc ttg gca gtt gtc ata gct tgt gca ggc gcc gtg acc ctc tcg aac 997
 Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn
 15 20 25

ttc cag ggc aag gtg atg atg acg gta aat gct act gac gtc aca gat 1045
 Phe Gln Gly Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp
 30 35 40 45

gtc atc acg att cca aca gct gct gga aag aac cta tgc att gtc aga 1093
 Val Ile Thr Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg
 50 55 60

gca atg gat gtg gga tac atg tgc gat gat act atc act tat gaa tgc 1141
 Ala Met Asp Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys
 65 70 75

cca gtg ctg tcg gct ggt aat gat cca gaa gac atc gac tgt tgg tgc 1189
 Pro Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys
 80 85 90

aca aag tca gca gtc tac gtc agg tat gga aga tgc acc aag aca cgc 1237
 Thr Lys Ser Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg
 95 100 105

cac tca aga cgc agt cgg agg tca ctg aca gtg cag aca cac gga gaa 1285
 His Ser Arg Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu
 110 115 120 125

agc act cta gcg aac aag aag ggg gct tgg atg gac agc acc aag gcc 1333
 Ser Thr Leu Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala
 130 135 140

aca agg tat ttg gta aaa aca gaa tca tgg atc ttg agg aac cct gga 1381
 Thr Arg Tyr Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly
 145 150 155

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Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr	
160 165 170	
atg cag aga gtt gtg ttt gtc gtg cta ttg ctt ttg gtg gcc cca gct	1477
Met Gln Arg Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala	
175 180 185	
tac agc ttc aac tgc ctt gga atg agc aac aga gac ttc ttg gaa gga	1525
Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly	
190 195 200 205	
gtg tct gga gca aca tgg gtg gat ttg gtt ctc gaa ggc gac agc tgc	1573
Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys	
210 215 220	
gtg act atc atg tct aag gac aag cct acc atc gat gtg aag atg atg	1621
Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met	
225 230 235	
aat atg gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg	1669
Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu	
240 245 250	
gct acc gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga	1717
Ala Thr Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly	
255 260 265	
gaa gct cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa	1765
Glu Ala His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln	
270 275 280 285	
gga gtg gtg gac agg ggc tgg ggc aac ggc tgc gga cta ttt ggc aaa	1813
Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys	
290 295 300	
gga agc att gac aca tgc gcc aaa ttt gcc tgc tct acc aag gca ata	1861
Gly Ser Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile	
305 310 315	
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Gly Arg Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe	
320 325 330	
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Val His Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln	
335 340 345	
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Val Gly Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro	
350 355 360 365	
tca tac aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt	2053

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Ser Tyr Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys	
370 375 380	
gaa cca cgg tca ggg att gac acc aat gca tac tac gtg atg act gtt	2101
Glu Pro Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val	
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Gly Thr Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn	
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Leu Pro Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr	
415 420 425	
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Leu Met Glu Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala	
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Leu Gly Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile	
450 455 460	
cct gtg gaa ttt tca agc aac act gtc aag ttg acg tcg ggt cat ttg	2341
Pro Val Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu	
465 470 475	
aag tgt aga gtg aag atg gaa aaa ttg cag ttg aag gga aca acc tat	2389
Lys Cys Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr	
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Gly Val Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr	
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ggt cac ggc act gtg gtg ttg gaa ttg cag tac act ggc acg gat gga	2485
Gly His Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly	
510 515 520 525	
cct tgc aaa gtt cct atc tcg tca gtg gct tca ttg aac gac cta acg	2533
Pro Cys Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr	
530 535 540	
cca gtg ggc aga ttg gtc act gtc aac cct ttt gtt tca gtg gcc acg	2581
Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr	
545 550 555	
gcc aac gct aag gtc ctg att gaa ttg gaa cca ccc ttt gga gac tca	2629
Ala Asn Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser	
560 565 570	
tac ata gtg gtg ggc aga gga gaa caa cag atc aat cac cat tgg cac	2677
Tyr Ile Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His	
575 580 585	

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 <211> 692
 <212> PRT
 <213> Artificial Sequence

<220>
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 synthetic construct

<223> pCBWN

<400> 16

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Lys	Val	Met	Met	Thr	Val	Asn	Ala	Thr	Asp	Val	Thr	Asp	Val	Ile	Thr
		35					40					45			
Ile	Pro	Thr	Ala	Ala	Gly	Lys	Asn	Leu	Cys	Ile	Val	Arg	Ala	Met	Asp
	50					55				60					
Val	Gly	Tyr	Met	Cys	Asp	Asp	Thr	Ile	Thr	Tyr	Glu	Cys	Pro	Val	Leu
65					70				75					80	
Ser	Ala	Gly	Asn	Asp	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	Thr	Lys	Ser
			85					90						95	
Ala	Val	Tyr	Val	Arg	Tyr	Gly	Arg	Cys	Thr	Lys	Thr	Arg	His	Ser	Arg
			100					105					110		
Arg	Ser	Arg	Arg	Ser	Leu	Thr	Val	Gln	Thr	His	Gly	Glu	Ser	Thr	Leu
		115					120					125			
Ala	Asn	Lys	Lys	Gly	Ala	Trp	Met	Asp	Ser	Thr	Lys	Ala	Thr	Arg	Tyr
	130					135					140				
Leu	Val	Lys	Thr	Glu	Ser	Trp	Ile	Leu	Arg	Asn	Pro	Gly	Tyr	Ala	Leu
145					150				155					160	
Val	Ala	Ala	Val	Ile	Gly	Trp	Met	Leu	Gly	Ser	Asn	Thr	Met	Gln	Arg
			165					170						175	
Val	Val	Phe	Val	Leu	Leu	Leu	Leu	Val	Ala	Pro	Ala	Tyr	Ser	Phe	
		180					185					190			
Asn	Cys	Leu	Gly	Met	Ser	Asn	Arg	Asp	Phe	Leu	Glu	Gly	Val	Ser	Gly
	195						200					205			

FOH0-SF3360

Ala	Thr	Trp	Val	Asp	Leu	Val	Leu	Glu	Gly	Asp	Ser	Cys	Val	Thr	Ile
210						215					220				
Met	Ser	Lys	Asp	Lys	Pro	Thr	Ile	Asp	Val	Lys	Met	Met	Asn	Met	Glu
225					230					235					240
Ala	Ala	Asn	Leu	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr	Leu	Ala	Thr	Val
				245					250					255	
Ser	Asp	Leu	Ser	Thr	Lys	Ala	Ala	Cys	Pro	Thr	Met	Gly	Glu	Ala	His
			260					265					270		
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		275					280					285			
Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile
		290				295						300			
Asp	Thr	Cys	Ala	Lys	Phe	Ala	Cys	Ser	Thr	Lys	Ala	Ile	Gly	Arg	Thr
305					310					315					320
Ile	Leu	Lys	Glu	Asn	Ile	Lys	Tyr	Glu	Val	Ala	Ile	Phe	Val	His	Gly
				325					330					335	
Pro	Thr	Thr	Val	Glu	Ser	His	Gly	Asn	Tyr	Ser	Thr	Gln	Val	Gly	Ala
			340					345					350		
Thr	Gln	Ala	Gly	Arg	Phe	Ser	Ile	Thr	Pro	Ala	Ala	Pro	Ser	Tyr	Thr
		355					360					365			
Leu	Lys	Leu	Gly	Glu	Tyr	Gly	Glu	Val	Thr	Val	Asp	Cys	Glu	Pro	Arg
		370				375					380				
Ser	Gly	Ile	Asp	Thr	Asn	Ala	Tyr	Tyr	Val	Met	Thr	Val	Gly	Thr	Lys
385					390					395					400
Thr	Phe	Leu	Val	His	Arg	Glu	Trp	Phe	Met	Asp	Leu	Asn	Leu	Pro	Trp
				405					410					415	
Ser	Ser	Ala	Gly	Ser	Thr	Val	Trp	Arg	Asn	Arg	Glu	Thr	Leu	Met	Glu
			420					425					430		
Phe	Glu	Glu	Pro	His	Ala	Thr	Lys	Gln	Ser	Val	Ile	Ala	Leu	Gly	Ser
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Gln	Glu	Gly	Ala	Leu	His	Gln	Ala	Leu	Ala	Gly	Ala	Ile	Pro	Val	Glu
						455					460				
Phe	Ser	Ser	Asn	Thr	Val	Lys	Leu	Thr	Ser	Gly	His	Leu	Lys	Cys	Arg
465					470					475					480
Val	Lys	Met	Glu	Lys	Leu	Gln	Leu	Lys	Gly	Thr	Thr	Tyr	Gly	Val	Cys
				485					490					495	
Ser	Lys	Ala	Phe	Lys	Phe	Leu	Gly	Thr	Pro	Ala	Asp	Thr	Gly	His	Gly
			500					505					510		
Thr	Val	Val	Leu	Glu	Leu	Gln	Tyr	Thr	Gly	Thr	Asp	Gly	Pro	Cys	Lys
			515				520					525			
Val	Pro	Ile	Ser	Ser	Val	Ala	Ser	Leu	Asn	Asp	Leu	Thr	Pro	Val	Gly
						535					540				
Arg	Leu	Val	Thr	Val	Asn	Pro	Phe	Val	Ser	Val	Ala	Thr	Ala	Asn	Ala
545					550					555					560
Lys	Val	Leu	Ile	Glu</											

Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
 645 650 655
 Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile
 660 665 670
 Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val
 675 680 685
 Asn Val His Ala
 690

<210> 17
 <211> 5334
 <212> DNA
 <213> Artificial Sequence

<220>
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 synthetic construct

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 <222> (916)...(3007)

<221> misc_feature
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 <223> pCBE 1-14

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 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
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 tctagagccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa 951
 Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
 1 5 10

ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg 999
 Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
 15 20 25

gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc 1047
 Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
 30 35 40

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Glu	Asn	Arg	Cys	Trp	Val	Arg	Ala	Ile	Asp	Val	Gly	Tyr	Met	Cys	Glu	
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Asp	Thr	Ile	Thr	Tyr	Glu	Cys	Pro	Lys	Leu	Thr	Met	Gly	Asn	Asp	Pro	
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Ser	Val	Gln	Thr	His	Gly	Glu	Ser	Ser	Leu	Val	Asn	Lys	Lys	Glu	Ala	
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Trp	Leu	Asp	Ser	Thr	Lys	Ala	Thr	Arg	Tyr	Leu	Met	Lys	Thr	Glu	Asn	
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Trp	Ile	Ile	Arg	Asn	Pro	Gly	Tyr	Ala	Phe	Leu	Ala	Ala	Val	Leu	Gly	
			160					165					170			
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Trp	Met	Leu	Gly	Ser	Asn	Asn	Gly	Gln	Arg	Val	Val	Phe	Thr	Ile	Leu	
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ctg	ctg	ttg	gtc	gct	cgg	gct	tac	agt	ttt	aat	tgt	ctg	gga	atg	ggc	1527
Leu	Leu	Leu	Val	Ala	Pro	Ala	Tyr	Ser	Phe	Asn	Cys	Leu	Gly	Met	Gly	
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205					210					215					220	
gtg	ctg	gaa	gga	gat	agc	tgc	ttg	aca	atc	atg	gca	aac	gac	aaa	cca	1623
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Val	Arg	Ser	Tyr	Cys	Tyr	His	Ala	Ser	Val	Thr	Asp	Ile	Ser	Thr	Val		
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Ala	Arg	Cys	Pro	Thr	Thr	Gly	Glu	Ala	His	Asn	Glu	Lys	Arg	Ala	Asp		
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T.D. 114-0332U3

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ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg 2439
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Thr	Thr	Gly	Glu	Ala	His	Asn	Glu	Lys	Arg	Ala	Asp	Ser	Ser	Tyr	Val
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Phe	Gly	Lys	Gly	Ser	Ile	Asp	Thr	Cys	Ala	Lys	Phe	Ser	Cys	Thr	Ser
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 Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
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<223> Description of artificial sequence; note =
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Asp	Gln	Thr	Ala	Val	Leu	Leu	Lys	Ser	Leu	Ala	Gly	Val	Pro	Leu	Ala		
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Gly	Asp	Leu	Ser	Gln	Gln	Trp	Phe	Gln	Lys	Gly	Ser	Thr	Ile	Gly	Arg		
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Met	Phe	Glu	Lys	Thr	Arg	Arg	Gly	Leu	Glu	Arg	Leu	Ser	Val	Val	Gly		
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ATTORNEY DOCKET NO. 14114.0332U3

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 Glu His Ala Trp Asp Phe Gly Ser Val Gly Gly Val Leu Ser Ser Val
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ggg aag gca atc cac acg gtg ctg ggg gga gct ttc aac acc ctt ttt 2823
 Gly Lys Ala Ile His Thr Val Leu Gly Gly Ala Phe Asn Thr Leu Phe
 625 630 635

ggg ggg gtt gga ttc atc cct aag atg ctg ctg ggg gtt gct ctg gtc 2871
 Gly Gly Val Gly Phe Ile Pro Lys Met Leu Leu Gly Val Ala Leu Val
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tgg ttg gga cta aat gcc agg aat cca acg atg tcc atg acg ttt ctt 2919
 Trp Leu Gly Leu Asn Ala Arg Asn Pro Thr Met Ser Met Thr Phe Leu
 655 660 665 670

gct gtg ggg gct ttg aca ctg atg atg aca atg gga gtt ggg gca t 2965
 Ala Val Gly Ala Leu Thr Leu Met Met Thr Met Gly Val Gly Ala
 675 680 685

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"ATTORNEY" AT 6:36:00

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<220>

<223> Description of artificial sequence; note =
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<400> 20

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Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser
        35        40        45
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       50       55       60
Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu
65          70          75          80
Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg
          85          90          95
Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg
        100        105        110
Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg
       115       120       125
Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu Gln Lys
      130      135      140
Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu
145          150          155          160
Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile
        165        170        175
Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile
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Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp
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Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro
     210     215     220
Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg
225          230          235          240
Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val
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Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu
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Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly
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14114-5-13300

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 305 310 315 320
 Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys
 325 330 335
 Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu
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 Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu
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 Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala
 370 375 380
 Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp
 385 390 395 400
 Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met
 405 410 415
 His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val
 420 425 430
 Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly
 435 440 445
 Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu
 450 455 460
 His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
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 Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
 485 490 495
 Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
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 Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
 515 520 525
 Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
 530 535 540
 Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
 545 550 555 560
 Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
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 Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
 580 585 590
 Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
 595 600 605
 Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
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 Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
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 Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
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<212> DNA

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<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (910)...(2986)

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gattattgac	tagttattaa	tagtaatcaa	ttacggggtc	attagttcat	agcccatata	300
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Gln Gly Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala	
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ata aac att cct agt gcc aac gga gca aac act tgc att gtg agg gct	1095
Ile Asn Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala	
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Leu Asp Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro	
65 70 75	

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Thr	Leu	Ala	Thr	Lys	Asn	Thr	Pro	Trp	Leu	Asp	Thr	Val	Lys	Thr	Thr		
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Lys	Tyr	Leu	Thr	Lys	Val	Glu	Asn	Trp	Val	Leu	Arg	Asn	Pro	Gly	Tyr		
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cag	aga	gtg	gtt	ttt	gtg	atc	atg	ctg	atg	ctg	att	gct	ccg	gca	tac		1479
Gln	Arg	Val	Val	Phe	Val	Ile	Met	Leu	Met	Leu	Ile	Ala	Pro	Ala	Tyr		
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Ser	Phe	Asn	Cys	Leu	Gly	Thr	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Ala		
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Ser	Gly	Ala	Thr	Trp	Ile	Asp	Leu	Val	Leu	Glu	Gly	Gly	Ser	Cys	Val		
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Met	Glu	Ala	Thr	Glu	Leu	Ala	Thr	Val	Arg	Glu	Tyr	Cys	Tyr	Glu	Ala		
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Val	Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly		
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Ser	Ile	Asp	Thr	Cys	Ala	Lys	Phe	Thr	Cys	Lys	Asn	Lys	Ala	Thr	Gly		
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aag	acg	atc	ttg	aga	gaa	aac	atc	aag	tat	gag	gtt	gca	atc	ttt	gtg		1911
Lys	Thr	Ile	Leu	Arg	Glu	Asn	Ile	Lys	Tyr	Glu	Val	Ala	Ile	Phe	Val		
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Gly Lys Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser
355 360 365

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Phe Thr Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu
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cca tgg acg agc cct gcc aca act gat tgg cgc aac aga gaa aca ctg 2199
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Gly Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro
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Ala Thr Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys
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Cys Arg Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly
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Met Cys Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly
495 500 505 510

cac ggg aca gtg att gtg gaa ctg cag tat act gga agc aac gga ccc 2487
His Gly Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro
515 520 525

tgc cga gtt ccc atc tcc gtg act gca aac ctc atg gat ttg aca ccg 2535
Cys Arg Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro
530 535 540

gtt gga aga ttg gtc acg gtc aat ccc ttt ata agc aca ggg gga gcg 2583

2025 RELEASE UNDER E.O. 14176

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Asn Asn Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr	
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atc gtc gtc gga aga ggc acc acc cag att aac tac cac tgg cac aaa	2679
Ile Val Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys	
575 580 585 590	
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Glu Gly Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala	
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Ala Thr Ser Val Gln Ala	
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14114.0332U3

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<212> PRT
<213> Artificial Sequence
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Lys	Val	Leu	Met	Ser	Ile	Asn	Lys	Thr	Asp	Ala	Gln	Ser	Ala	Ile	Asn
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Ile	Pro	Ser	Ala	Asn	Gly	Ala	Asn	Thr	Cys	Ile	Val	Arg	Ala	Leu	Asp
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Ser	Ala	Gly	Asn	Asp	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	Asp	Val	Glu
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Glu	Val	Trp	Val	His	Tyr	Gly	Arg	Cys	Thr	Arg	Met	Gly	His	Ser	Arg
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 145 150 155 160
 Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr Gln Arg
 165 170 175
 Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr Ser Phe
 180 185 190
 Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser Gly
 195 200 205
 Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr Val
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 Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro Cys Arg
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 Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val Gly
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14114.0332U3
 ATTORNEY DOCKET NO.

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<212> DNA
<213> Artificial Sequence

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<221> CDS
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Asn	Arg	Trp	Leu	Leu	Asn	Val	Thr	Ser	Glu	Asp	Leu	Gly	Lys	Thr		
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Phe	Ser	Val	Gly	Thr	Gly	Asn	Cys	Thr	Thr	Asn	Ile	Leu	Glu	Ala	Lys	
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Tyr	Trp	Cys	Pro	Asp	Ser	Met	Glu	Tyr	Asn	Cys	Pro	Asn	Leu	Ser	Pro	
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Arg	Glu	Glu	Pro	Asp	Asp	Ile	Asp	Cys	Trp	Cys	Tyr	Gly	Val	Glu	Asn	
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- 1. The first part of the document is a list of references. The references are listed in a vertical column on the left side of the page. The references are:

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 50 55 60
 Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu
 65 70 75 80
 Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg
 85 90 95
 Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg
 100 105 110
 Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg
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 Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu Gln Lys
 130 135 140
 Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu
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 Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile
 165 170 175
 Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile
 180 185 190
 Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp
 195 200 205
 Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro
 210 215 220
 Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg
 225 230 235 240
 Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val
 245 250 255
 Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu
 260 265 270
 Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly
 275 280 285
 Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys
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 Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln
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 370 375 380
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 405 410 415
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 420 425 430
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Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu
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His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
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Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
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Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
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Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
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Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
530 535 540
Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
545 550 555 560
Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
565 570 575
Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
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Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
595 600 605
Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
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Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
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Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
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<223> Modified JE Signal

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<223> YF 482

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44-ATT-3360

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<210> 31
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40

2010-07-23 00:00